

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/882,431DATE: 02/09/98  
TIME: 11:29:54

INPUT SET: S23303.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

#4

## SEQUENCE LISTING

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FEB 26 1998

PATENT DEPARTMENT

JOHN MORAN-PATENT ATTORNEY

1  
2  
3 (1) General Information:  
4 (i) APPLICANT: Robert G. Ulrich,  
5 Mark A. Olson  
6 Sina Bavari  
7  
8 (ii) TITLE OF INVENTION: Bacterial Superantigen  
9 Vaccines  
10  
11 (iii) NUMBER OF SEQUENCES:16  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: John Moran  
15 (B) STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)  
16 (C) CITY: FORT DETRICK  
17 (D) STATE: MARYLAND  
18 (E) COUNTRY: USA  
19 (F) ZIP: 21702-5012  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: Apple Macintosh  
24 (C) OPERATING SYSTEM: Macintosh 7.5  
25 (D) SOFTWARE: Microsoft Word 6.0  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: 08/882,431  
29 (B) FILING DATE: June 25, 1997  
30 (C) CLASSIFICATION:  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER:  
34 (B) FILING DATE:  
35  
36 (viii) ATTORNEY/AGENT INFORMATION:  
37 (A) NAME: Moran, John  
38 (B) REGISTRATION NUMBER: 26,313  
39 (C) REFERENCE/DOCKET NUMBER:  
40  
41 (ix) TELECOMMUNICATION INFORMATION  
42 (A) TELEPHONE: (301) 619-2065  
43 (B) TELEFAX: (301) 619-7714  
44  
45 (2) INFORMATION FOR SEQ ID NO:1:  
46 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 830  
48 (B) TYPE: Nucleic Acid  
49 (C) STRANDEDNESS: Unknown  
50 (D) TOPOLOGY: Unknown  
51 (ii) MOLECULE TYPE: DNA  
52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
53  
54 atgaaaaaaaa cagcatttac attactttta ttcattgccc 40  
55  
56 taacgttgac aacaagtcca cttgtaaatg gtagcgagaa 80  
57  
58 aagcgaagaa ataaatgaaa aagatttgcg aaaaaagtct 120  
59  
60 gaattgcagg gaacagcttt aggcaatctt aaacaaatct 160  
61  
62 attattacaa tgaaaaagct aaaactgaaa ataaagagag 200  
63  
64 tcacgatcaa tttcgacagc atactatatt gtttaaaggc 240  
65  
66 ttttttacag atcattcgtg gtataacgat ttattagtag 280  
67  
68 gttttgattc aaaggatatt gttgataaat ataaagggaa 320  
69  
70 aaaagtagac ttgtatggtg cttatgctgg ttatcaatgt 360  
71  
72 gcgggtggtg caccaaacia aacagcttgt atgtatggtg 400  
73  
74 gtgtaacgtt acatgataat aatcgattga ccgaagagaa 440  
75  
76 aaaagtgccg atcaatttat ggctagacgg taaacaaaat 480  
77  
78 acagtacctt tggaaacggt taaaacgaat aagaaaaatg 520  
79  
80 taactgttca ggagttggat cttcaagcaa gacgttattt 560  
81  
82 acaggaaaaa tataatttat ataactctga tgtttttgat 600  
83  
84 gggaagggtc agaggggatt aatcgtgttt catacttcta 640  
85  
86 cagaaccttc ggttaattac gatttatttg gtgtcaagg 680  
87  
88 acagtattca aatacactat taagaatata tagagataat 720  
89  
90 aaaacgatta actctgaaaa catgcatatt gatatatatt 760  
91  
92 tatatacaag ttaaACATGG TAGTTTGTGAC CAACGTAATG 800  
93  
94 TTCAGATTAT TATGAACCGA GAATAATCTA 830  
95  
96 (2) INFORMATION FOR SEQ ID NO:2:  
97 (i) SEQUENCE CHARACTERISTICS:  
98 (A) LENGTH: 257  
99 (B) TYPE: Amino Acid

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100 (C) STRANDEDNESS: Unknown  
101 (D) TOPOLOGY: Unknown  
102 (ii) MOLECULE TYPE: Peptide  
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
104  
105 Met Lys Lys Thr Ala Phe Thr Leu Leu Leu  
106 1 5 10  
107  
108 Phe Ile Ala Leu Thr Leu Thr Thr Ser Pro  
109 15 20  
110  
111 Leu Val Asn Gly Ser Glu Lys Ser Glu Glu  
112 25 30  
113  
114 Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser  
115 35 40  
116  
117 Glu Lys Gln Gly Thr Ala Leu Gly Asn Leu  
118 45 50  
119  
120 Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala  
121 55 60  
122  
123 Lys Thr Glu Asn Lys Glu Ser His Asp Gln  
124 65 70  
125  
126 Phe Arg Gln His Thr Ile Leu Phe Lys Gly  
127 75 80  
128  
129 Phe Phe Thr Asp His Ser Trp Tyr Asn Asp  
130 85 90  
131  
132 Leu Leu Val Arg Phe Asp Ser Lys Asp Ile  
133 95 100  
134  
135 Val Asp Lys Tyr Lys Gly Lys Lys Val Asp  
136 105 110  
137  
138 Leu Tyr Gly Ala Tyr Ala Gly Tyr Gln Cys  
139 115 120  
140  
141 Ala Gly Gly Thr Phe Asn Lys Thr Ala Cys  
142 125 130  
143  
144 Met Tyr Gly Gly Val Thr Leu His Asp Asn  
145 135 140  
146  
147 Asn Arg Leu Thr Glu Glu Lys Lys Val Pro  
148 145 150  
149  
150 Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn  
151 155 160  
152

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153 Thr Val Pro Leu Glu Thr Val Lys Thr Asn
154                               165                170
155
156 Lys Lys Asn Val Thr Val Gln Glu Leu Asp
157                               175                180
158
159 Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys
160                               185                190
161
162 Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
163                               195                200
164
165 Gly Lys Val Gln Arg Gly Leu Ile Val Phe
166                               205                210
167
168 His Thr Ser Thr Glu Pro Ser Val Asn Tyr
169                               215                220
170
171 Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser
172                               225                230
173
174 Asn Thr Leu leu Arg Ile Tyr Arg Asp Asn
175                               235                240
176
177 Lys Thr Ile asn Ser Glu Asn Met His Ile
178                               245                250
179
180 Asp Ile Tyr Leu Tyr Thr Ser
181                               255
182

```

183 (2) INFORMATION FOR SEQ ID NO:3:

184 (i) SEQUENCE CHARACTERISTICS:

185 (A) LENGTH: 757

186 (B) TYPE: Nucleic Acid

187 (C) STRANDEDNESS: Unknown

188 (D) TOPOLOGY: Unknown

189 (ii) MOLECULE TYPE: DNA

190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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191
192 atgagaaaag cgaagaaata aatgaaaaag atttgcgaaa      40
193
194 aaagtctgaa ttgcagggaa cagctttagg caatcttaaa      80
195
196 Caaatctatt attacaatga aaaagctaaa actgaaaata     120
197
198 aagagagtca cgatcaattt cgacagcata ctatattggt     160
199
200 taaaggcttt ttacagatc attcgtggta taacgattta     200
201
202 ttagtacgtt ttgattcaaa ggatattggt gataaatata     240
203
204 aagggaaaaa agtagacttg tatggtgctt atgctggtta     280
205

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206 tcaatgtgcg ggtggtacac caaacaaaac agcttgtatg 320
207
208 tatggtggtg taacgttaca tgataataat cgattgaccg 360
209
210 aagagaaaaa agtgccgatc aatttatggc tagacggtaa 400
211
212 acaaaatata gtacctttgg aaacgggttaa aacgaataag 440
213
214 aaaaatgtaa ctgttcagga gttggatctt caagcaagac 480
215
216 gttattttaca ggaaaaatat aatttatata actctgatgt 520
217
218 ttttgatggg aaggttcaga ggggattaat cgtgtttcat 560
219
220 acttctacag aaccttcggt taattacgat ttatttggtg 600
221
222 ctcaaggaca gtattcaaat acactattaa gaatatatag 640
223
224 agataataaaa acgattaact ctgaaaacat gcatattgat 680
225
226 atatatttat atacaagtta aACATGGTAG TTTTGACCAA 720
227
228 CGTAATGTTC AGATTATTAT GAACCGAGAA TAATCTA 757
229
230 (2) INFORMATION FOR SEQ ID NO:4:
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH:233
233 (B) TYPE: Amino Acid
234 (C) STRANDEDNESS: Unknown
235 (D) TOPOLOGY: Unknown
236 (ii) MOLECULE TYPE: Peptide
237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
238
239 Met Glu Lys Ser Glu Glu Ile Asn Glu Lys
240 5 10
241
242 Asp Leu Arg Lys Lys Ser Glu Lys Gln Gly
243 15 20
244
245 Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr
246 25 30
247
248 Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
249 35 40
250
251 Lys Glu Ser His Asp Gln Phe Arg Gln His
252 45 50
253
254 Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp
255 55 60
256
257 His Ser Trp Tyr Asn Asp Leu Leu Val Arg
258 65 70

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**SEQUENCE VERIFICATION REPORT**  
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